

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 28, 2002, 17:40:15 ; Search time 63.43 Seconds

(without alignments)
575.468 Million cell updates/sec

Title: US-09-502-984B-6
Perfect score: 1098
Sequence: 1 KFESKALLAARGPPELLCF.....AEPGFGGFWASMSPEVSULT 211

Scoring table:
BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_19:*
1: sp-archaea:*
2: sp-bacteria:*
3: sp-fungi:*
4: sp-human:*
5: sp-invertebrate:*
6: sp-mammal:*
7: sp-mhc:*
8: sp-organelle:*
9: sp-phage:*
10: sp-plant:*
11: sp-rodent:*
12: sp-virus:*
13: sp-vertebrate:*
14: sp-unclassified:*
15: sp-virus:*
16: sp-bacteriap:*
17: sp-archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-----------|--------------------|
| 1 | 903.5 | 82.3 | 509 | Q9MYZ9 | Q9MYZ9 sus scrofa |
| 2 | 877.5 | 79.9 | 316 | 11 Q35545 | Q35545 rattus norv |
| 3 | 782 | 71.2 | 229 | 6 Q27950 | Q27950 bos indicus |
| 4 | 778 | 70.9 | 229 | 6 Q28206 | Q28206 bos taurus |
| 5 | 719.5 | 65.5 | 387 | 6 Q95N13 | Q95N13 ovis aries |
| 6 | 719.5 | 65.5 | 418 | 6 Q95N14 | Q95N14 ovis aries |
| 7 | 152 | 13.8 | 566 | 11 Q925F5 | Q925F5 mus musculu |
| 8 | 122.5 | 11.2 | 422 | 4 Q75462 | Q75462 homo sapien |
| 9 | 121.5 | 11.1 | 422 | 4 Q90H5 | Q90H5 homo sapien |
| 10 | 119.5 | 10.9 | 296 | 6 Q18880 | Q18880 mus musculu |
| 11 | 118 | 10.7 | 296 | 6 Q18880 | Q18880 bos taurus |
| 12 | 112.5 | 10.2 | 581 | 6 Q46561 | Q46561 ovis aries |
| 13 | 112.5 | 10.2 | 634 | 6 Q46600 | Q46600 bos taurus |
| 14 | 111.5 | 10.2 | 626 | 13 Q90WG7 | Q90WG7 cynops pyr |
| 15 | 111 | 10.1 | 521 | 4 Q96TF0 | Q96TF0 homo sapien |
| 16 | 105.5 | 9.6 | 638 | 6 Q95JF2 | Q95JF2 alluropoda |

| | | | | | |
|----|-------|-----|------|-----------|---------------------|
| 17 | 104.5 | 9.5 | 608 | 6 Q9N0Y7 | Q9N0Y7 monodelphis |
| 18 | 102.5 | 9.3 | 628 | 11 Q9JKT1 | Q9JKT1 cavia porce |
| 19 | 102.5 | 9.3 | 628 | 11 Q9JKT1 | Q9JKT1 cavia porce |
| 20 | 102.5 | 9.3 | 628 | 11 Q9JKT1 | Q9JKT1 cavia porce |
| 21 | 101.5 | 9.2 | 848 | 6 Q9M2S2 | Q9M2S2 sus scrofa |
| 22 | 99.5 | 9.1 | 1165 | 6 Q02671 | Q02671 sus scrofa |
| 23 | 99 | 9.0 | 622 | 6 Q9N0J7 | Q9N0J7 callithrix |
| 24 | 99 | 9.0 | 894 | 6 Q9MYL1 | Q9MYL1 macaca mula |
| 25 | 99 | 9.0 | 925 | 6 Q9MYK9 | Q9MYK9 macaca mula |
| 26 | 99 | 9.0 | 1163 | 6 Q9MYL2 | Q9MYL2 macaca mula |
| 27 | 99 | 9.0 | 1194 | 6 Q9MYL0 | Q9MYL0 macaca mula |
| 28 | 98 | 8.9 | 538 | 4 Q9HBE5 | Q9HBE5 homo sapien |
| 29 | 98 | 8.9 | 538 | 4 Q9HB91 | Q9HB91 homo sapien |
| 30 | 96.5 | 8.8 | 390 | 4 Q9UEH7 | Q9UEH7 homo sapien |
| 31 | 96.5 | 8.8 | 638 | 6 Q9TUE9 | Q9TUE9 canis famill |
| 32 | 96.5 | 8.8 | 1093 | 11 Q70535 | Q70535 rattus norv |
| 33 | 96 | 8.7 | 896 | 4 Q92919 | Q92919 homo sapien |
| 34 | 96 | 8.7 | 896 | 4 Q13594 | Q13594 homo sapien |
| 35 | 96 | 8.7 | 906 | 4 Q13593 | Q13593 homo sapien |
| 36 | 96 | 8.7 | 958 | 4 Q92920 | Q92920 homo sapien |
| 37 | 96 | 8.7 | 958 | 4 Q13592 | Q13592 homo sapien |
| 38 | 96 | 8.7 | 1165 | 4 Q92921 | Q92921 homo sapien |
| 39 | 95.5 | 8.7 | 611 | 13 Q9PTR9 | Q9PTR9 xenopus lae |
| 40 | 95.5 | 8.7 | 636 | 13 Q90216 | Q90216 parailichthy |
| 41 | 94.5 | 8.6 | 615 | 13 Q9DE35 | Q9DE35 pelodiscus |
| 42 | 94.5 | 8.6 | 632 | 6 Q95ML5 | Q95ML5 salmirt hol |
| 43 | 93 | 8.5 | 227 | 6 Q9CLW3 | Q9CLW3 ursus marit |
| 44 | 91 | 8.3 | 608 | 11 Q99JZ1 | Q99JZ1 mus musculu |
| 45 | 90 | 8.2 | 229 | 4 Q14213 | Q14213 homo sapien |

ALIGNMENTS

| RESULT | ID | PRELIMINARY | PRT | 509 AA. |
|--------|---|-------------|-----|---------|
| Q9MYZ9 | Q9MYZ9 | | | |
| AC | Q9MYZ9 | | | |
| DT | 01-OCT-2000 (TREMBLREL. 15, Created) | | | |
| DT | 01-OCT-2000 (TREMBLREL. 15, Last sequence update) | | | |
| DE | 01-DEC-2001 (TREMBLREL. 19, Last annotation update) | | | |
| DE | ERYTHROPOIETIN RECEPTOR. | | | |
| OS | sus scrofa (pig). | | | |
| OC | Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus. | | | |
| OX | NCBI_TaxID=9823; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | TISSUE=LIVER; | | | |
| RA | Pearson P.L., Smith T.P.L., Sonstegard T.S., Klemcke H.G., | | | |
| RA | Christenson R.K., Vallet J.L., | | | |
| RT | "Porcine Erythropoietin Receptor: Molecular Cloning and Expression in | | | |
| RT | Embryonic and Fetal Liver." | | | |
| RL | Domest. Anim. Endocrinol. 0:0-0(2000). | | | |
| DR | EMBL; AF274305; AAF77065.1; - | | | |
| DR | HSSP; P19235; 1EBA. | | | |
| DR | InterPro; IPR002966; CRA. | | | |
| DR | InterPro; IPR000572; Euk_oxidored_molyb. | | | |
| DR | InterPro; IPR003961; FN_III. | | | |
| DR | InterPro; IPR003528; Hematopo_receptor_L_F1. | | | |
| DR | Pfam; PF00041; fn3; 1. | | | |
| DR | SMART; SM00060; FN3; 1. | | | |
| DR | PROSITE; PS01352; HEMATOPO_REC_L_F1; UNKNOWN_1. | | | |
| DR | PROSITE; PS00559; MOLYBDOPTERIN_EUK; UNKNOWN_1. | | | |
| DR | RECEPTOR. | | | |
| SQ | SEQUENCE 509 AA; 55183 MW; 35B565D07C6BCD8A CRC64; | | | |

Query Match 82.3%; Score 903.5; DB 6; Length 509;
Best Local Similarity 80.2%; Pred. No. 3.7e-79;
Matches 170; Conservative 18; Mismatches 23; Indels 1; Gaps 1;
QY 1 KFESKALLAARGPPELLCFTEHRLDLVCFPEEASAGVPGNFSFQLDEBPMKRLCTL 60

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Db      34 KFESKALLAARGPEELCFERLEEDLVCFWEESAGSAGVGEDYSFSYQLEGEPMKPCHL 93
QY      61 HOAPTANGALRFWCSLTADTSSVPLLELRT-AASGAPRHRVHIHNEVLLDAPGLV 119
Db      94 HOGTANGSVRFWCSLTADTSSVPLLELRTVEVSGAPRHRVHIHNEVLLDPPAGLL 153
QY      120 ARLADESGHVIRWLPPEPTMTSHIRFELDLSAGNGASVORVELLEGRTCVLSNLRG 179
Db      154 ARREESGHHVLRWLPPEPPAPMALSIRYEVNISREMAAGVQRVEILLDGRTECVLSNLRG 213
QY      180 RTRITIAVRARMAEPSPFGGFWMSAMSEVSLT 211
Db      214 GTRTYFMVRRARMAEPSPFGGFWMSAMSEPASILT 245

RESULT  2
ID      035545 PRELIMINARY; PRT; 316 AA.
AC      035545;
DT      01-JAN-1998 (TEMBLrel. 05, Created)
DT      01-JAN-1998 (TEMBLrel. 05, Last sequence update)
DT      01-DEC-2001 (TEMBLrel. 19, Last annotation update)
DE      INTRON 5-INSERTED FORM OF ERYTHROPOIETIN RECEPTOR PRECURSOR.
OS      Rattus norvegicus (Rat).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
ON      NCBI_TaxID=10116;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=98296111; PubMed=9630610;
RA      Yamaji R., Murakami C., Takenoshita M., Tsuyama S., Inui H.,
RA      Miyatake K., Nakano Y.;
RT      "The intron 5-inserted form of rat erythropoietin receptor is
RT      expressed as a membrane-bound form.";
RL      Blochim. Biophys. Acta 1403:169-176(1998).
DR      EMBL: D83509; BAA22373.1; -.
DR      HSSP: P19235; IEBA.
DR      InterPro: IPR002996; CRIA.
DR      InterPro: IPR003961; FN.III.
DR      InterPro: IPR003528; Hematopo_receptor_L.F1.
DR      Pfam: PF00041; fn3; 1.
DR      SMART: SM00060; FN3; 1.
DR      PROSITE: PS01352; HEMATOPO_REC_L.F1; UNKNOWN_1.
KW      Signal; Receptor.
FT      SIGNAL 1 24 POTENTIAL.
FT      CHAIN 25 316 POTENTIAL.
SQ      SEQUENCE 316 AA; 34220 MW; 05C44B8516C180B CRC64;

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Query Match 79.9%; Score 877.5; DB 11; Length 316;
 Best Local Similarity 78.2%; Pred. No. 6.8e-77;
 Matches 165; Conservative 23; Mismatches 22; Indels 1; Gaps 1;

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QY      1 KFESKALLAARGPEELCFERLEEDLVCFWEESAGSAGVGEDYSFSYQLEGEPMKPCRL 60
Db      34 KFESKALLAARGPEELCFERLEEDLVCFWEESAGSAGVGEDYSFSYQLEGEPMKPCRL 92
QY      61 HOAPTANGALRFWCSLTADTSSVPLLELRTAASGAPRHRVHIHNEVLLDAPGLV 120
Db      94 HOGTANGSVRFWCSLTADTSSVPLLELRTVEVSGAPRHRVHIHNEVLLDPPAGLL 152
QY      121 ARLADESGHVIRWLPPEPTMTSHIRFELDLSAGNGASVORVELLEGRTCVLSNLGR 180
Db      153 ARREESGHHVLRWLPPEPPAPMALSIRYEVNISREMAAGVQRVEILLDGRTECVLSNLRG 212
QY      181 RTRITIAVRARMAEPSPFGGFWMSAMSEVSLT 211
Db      213 GTRTYFMVRRARMAEPSPFGGFWMSAMSEPASILT 243

RESULT  3
Q27950

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ID      Q27950 PRELIMINARY; PRT; 229 AA.
AC      Q27950;
DT      01-NOV-1996 (TEMBLrel. 01, Created)
DT      01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DT      01-DEC-2001 (TEMBLrel. 19, Last annotation update)
DE      ERYTHROPOIETIN RECEPTOR (FRAGMENT).
GN      EPOR.
OS      Bos indicus (Zebu).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC      Bovidae; Bovinae; Bos.
ON      NCBI_TaxID=9913;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=BONE MARROW;
RA      Sullivan H.B., Feldman B.F., Majiwa P.A.O., Logan-Henfrey L.L.;
RL      Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR      EMBL: U61398; AAB03870.1; -.
DR      HSSP: P19235; IEBA.
DR      InterPro: IPR002996; CRIA.
DR      InterPro: IPR003961; FN.III.
DR      InterPro: IPR003528; Hematopo_receptor_L.F1.
DR      Pfam: PF00041; fn3; 1.
DR      SMART: SM00060; FN3; 1.
DR      PROSITE: PS01352; HEMATOPO_REC_L.F1; UNKNOWN_1.
KW      Receptor.
FT      NON_TER 1 1
FT      NON_TER 229 229
SQ      SEQUENCE 229 AA; 25196 MW; F6E01CAAB07893E8 CRC64;

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Query Match 71.2%; Score 782; DB 6; Length 229;
 Best Local Similarity 78.5%; Pred. No. 8.1e-68;
 Matches 146; Conservative 15; Mismatches 25; Indels 0; Gaps 0;

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QY      26 DLVCFEEBASAGVPGNFSFSLDEDEPMKICLHQAPTARGAIRRWCSLPTADTSSV 85
Db      1 DLVCFEBAATAGVGPDPNYSFSYQLEGEPMKPCRLHQAPTARGLVRFWCSLPTADTSSV 60
QY      86 PLELRTAASGAPRHRVHIHNEVLLDAPGLVARLADSGHVIRWLPPEPTMTSHI 145
Db      61 PLELHTAASGASIKRTIHYNEVLLDPPARLVARRADESGHVLRWLPPEPPAPMALSIL 120
QY      146 RFEILDLSAGNGASVORVELLEGRTCVLSNLGRTRITIAVRARMAEPSPFGGFWMSAMSE 205
Db      121 RYEVNISAEVNAAGSAQVREILLDGRTECLLSNLRGTRTYFMVRRARMAEPSPFGGFWMSAMSE 180
QY      206 PVSLT 211
Db      181 PASILT 186

RESULT  4
Q28206
ID      Q28206 PRELIMINARY; PRT; 229 AA.
AC      Q28206;
DT      01-NOV-1996 (TEMBLrel. 01, Created)
DT      01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DT      01-DEC-2001 (TEMBLrel. 19, Last annotation update)
DE      ERYTHROPOIETIN RECEPTOR (FRAGMENT).
GN      EPOR.
OS      Bos taurus (Bovine).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC      Bovidae; Bovinae; Bos.
ON      NCBI_TaxID=9913;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=BONE MARROW;
RA      Sullivan H.B., Feldman B.F., Majiwa P.A.O., Logan-Henfrey L.L.;
RL      Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR      EMBL: U61399; AAB03871.1; -.
DR      HSSP: P19235; IEBA.

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[illegible]

DR EMBL: AF041357; AAB966795.1; -
DR EMBL: AF041977; AAB966920.1; -
DR EMBL: AF041979; AAB97082.1; -
DR EMBL: AF042358; AAB97744.1; -
DR EMBL: AF042258; AAB97743.1; -
DR EMBL: AF041978; AAB956965.1; -
DR EMBL: Y10578; CAAT1597.1; -
DR EMBL: Y10808; CAAT1766.1; -
DR HSSP: P14787; IAN3.
DR InterPro: IPR002936; CRAA.
DR InterPro: IPR003961; FN.III.
DR InterPro: IPR003528; Hematopo_receptor_L.F1.
DR Pfam: PF00041; fn3; 2.
DR SMART: SM00060; FN3; 2.
DR PROSITE: PS013302; HEMATOPO_REC_L.F1; UNKNOWN.1

DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE INTERLEUKIN 9 RECEPTOR.
 GN IL9R.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20122249; PubMed=10655549;
 RA Ciccodicola A., D'Esposito M., Esposito T., Gianfrancesco F.,
 RA Migliaccio C., Milano M.G., Matarazzo M.R., Vacca M., Franze A.,
 RA Cucurese M., Cocchia M., Curci A., Terracciano A., Torino A.,
 RA Cocchia S., Mercadante G., Pannone E., Archidiacono N., Rocchi M.,
 RA Schlessinger D., D'Urso M.;
 RT "Differentially regulated and evolved genes in the fully sequenced
 RT Xq/Yq pseudautosomal region.";
 RL Hum. Mol. Genet. 9:395-401(2000).
 DR EMBL: AJ271736; CAB96817.1; -.
 KW Receptor.
 SQ SEQUENCE 521 AA: 57146 MW: 07C40436466173F3 CRC64;

Query Match 10.1%; Score 111; DB 4; Length 521;
 Best Local Similarity 23.7%; Pred. No. 0.019; Indels 46; Gaps 11;
 Matches 53; Conservative 28; Mismatches 97;

OY 12 RGPEE-LLCFTELEDLVCFEEAASAGVGPNGFSFQLEDEPWKLCRLHQAPTARGA 69
 DB 47 QGPRSRTEFTCLNNILRIDCHW-SAPELGQ-----SSPWLFSTNQAPGTHK 94
 OY 70 IFNCSLPFADTSSVPELERLTAAG-APRRHYIHNEV-----VLLDAP 115
 DB 95 ---CILRGSECTVVLPEAVLVPDSNFTTTEHHCMGSGREQVSLVDPEYLPRRHVKLDPP 150
 OY 116 VGLVARLADSGHVVIRW-LPPETPMTSHIRFELDLSAGNGA-GSVORVELLEGTECV 173
 DB 151 SDLOSNIIS--SGHCILTWISIPALEPMTLLSYELAFKKOEKAWEOAQHRDHIVGVTWLI 208
 OY 174 LSNL-----RGRRTITIAVRAR--MAEPSGFGFWSAMSEPV 207
 DB 209 LEAFELDPGFIEARLRVQMATLEDVVEEERYTGQWSEWQPV 252

Search completed: August 28, 2002, 17:40:15
 Job time: 546 sec

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